



SEQUENCE LISTING

<110> Yanofsky, Martin F.
Pelaz, Soraya
Ditta, Gary
The Regents of the University of California

<120> Combinations of Genes for Producing Seed Plants
Exhibiting Modulated Reproductive Development

<130> 19452A-002400US

<140> US 09/853,450

<141> 2001-05-09

<160> 61

<170> PatentIn Ver. 2.1

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aaa atg gga agg ggt agg gtt caa ttg aag agg ata gag aac aag atc 168
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Asn Arg Gln Val Thr Phe Ser Lys Arg Arg Ala Gly Leu Leu Lys Lys
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gct cat gag atc tct gtt ctc tgt gat gct gaa gtt gct ctt gtt gtc 264
Ala His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Val
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Phe Ser His Lys Gly Lys Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met
50 55 60
gag aag ata ctt gaa cgc tat gag agg tac tct tac gcc gaa aga cag 360
Glu Lys Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Arg Gln
65 70 75
ctt att gca cct gag tcc gac gtc aat aca aac tgg tcg atg gag tat 408
Leu Ile Ala Pro Glu Ser Asp Val Asn Thr Asn Trp Ser Met Glu Tyr
80 85 90 95
aac agg ctt aag gct aag att gag ctt ttg gag aga aac cag agg cat 456
Asn Arg Leu Lys Ala Lys Ile Glu Leu Leu Glu Arg Asn Gln Arg His
100 105 110

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Tyr Leu Gly Gln Asp Leu Gln Ala Met Ser Pro Lys Glu Leu Gln Asn	
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ctg gag cag cag ctt gac act gct ctt aag cac atc cgc act aga aaa	552
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145 150 155	
gcc ata cag gag caa aac agc atg ctt tct aaa cag atc aag gag agg	648
Ala Ile Gln Glu Gln Asn Ser Met Leu Ser Lys Gln Ile Lys Glu Arg	
160 165 170 175	
gaa aaa att ctt agg gct caa cag gag cag tgg gat cag cag aac caa	696
Glu Lys Ile Leu Arg Ala Gln Gln Glu Gln Trp Asp Gln Gln Asn Gln	
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ggc cac aat atg cct ccc cct ctg cca ccg cag cag cac caa atc cag	744
Gly His Asn Met Pro Pro Pro Leu Pro Pro Gln Gln His Gln Ile Gln	
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Gly Leu Tyr Gln Glu Asp Asp Pro Met Ala Met Arg Arg Asn Asp Leu	
225 230 235	
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Glu Leu Thr Leu Glu Pro Val Tyr Asn Cys Asn Leu Gly Cys Phe Ala	
240 245 250 255	
gca tga agcatttcca tatatatatt tgtaatcgtc aacaataaaa acagtttgcc	944
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 35 40 45
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 50 55 60

Lys Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Arg Gln Leu
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 85 90 95
 Arg Leu Lys Ala Lys Ile Glu Leu Leu Glu Arg Asn Gln Arg His Tyr
 100 105 110
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 115 120 125
 Glu Gln Gln Leu Asp Thr Ala Leu Lys His Ile Arg Thr Arg Lys Asn
 130 135 140
 Gln Leu Met Tyr Glu Ser Ile Asn Glu Leu Gln Lys Lys Glu Lys Ala
 145 150 155 160
 Ile Gln Glu Gln Asn Ser Met Leu Ser Lys Gln Ile Lys Glu Arg Glu
 165 170 175
 Lys Ile Leu Arg Ala Gln Gln Glu Gln Trp Asp Gln Gln Asn Gln Gly
 180 185 190
 His Asn Met Pro Pro Leu Pro Pro Gln Gln His Gln Ile Gln His
 195 200 205
 Pro Tyr Met Leu Ser His Gln Pro Ser Pro Phe Leu Asn Met Gly Gly
 210 215 220
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 Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn Arg Gln Val Thr Phe Ser
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 aaa aga aga gct ggt ctt atg aag aaa gct cat gag atc tct gtt ctg 149
 Lys Arg Arg Ala Gly Leu Met Lys Lys Ala His Glu Ile Ser Val Leu
 25 30 35

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 Cys Asp Ala Glu Val Ala Leu Val Val Phe Ser His Lys Gly Lys Leu
 40 45 50

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 Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu Lys Ile Leu Glu Arg Tyr
 55 60 65 70

 gag aga tac tct tac gcc gag aga cag ctt ata gca cct gag tcc gac 293
 Glu Arg Tyr Ser Tyr Ala Glu Arg Gln Leu Ile Ala Pro Glu Ser Asp
 75 80 85

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Ser Asn Thr Asn Trp Ser Met Glu Tyr Asn Arg Leu Lys Ala Lys Ile	
90 95 100	
gag ctt ttg gag aga aac cag agg cac tat ctt ggg gaa gac ttg caa	389
Glu Leu Leu Glu Arg Asn Gln Arg His Tyr Leu Gly Glu Asp Leu Gln	
105 110 115	
gca atg agc cct aag gaa ctc cag aat cta gag caa cag ctt gat act	437
Ala Met Ser Pro Lys Glu Leu Gln Asn Leu Glu Gln Leu Asp Thr	
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gct ctt aag cac atc cgc tct aga aaa aac caa ctt atg tac gac tcc	485
Ala Leu Lys His Ile Arg Ser Arg Lys Asn Gln Leu Met Tyr Asp Ser	
135 140 145 150	
atc aat gag ctc caa aga aag gag aaa gcc ata cag gaa caa aac agc	533
Ile Asn Glu Leu Gln Arg Lys Glu Lys Ala Ile Gln Glu Gln Asn Ser	
155 160 165	
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Met Leu Ser Lys Gln Ile Lys Glu Arg Glu Asn Val Leu Arg Ala Gln	
170 175 180	
caa gag caa tgg gac gag cag aac cat ggc cat aat atg cct ccg cct	629
Gln Glu Gln Trp Asp Glu Gln Asn His Gly His Asn Met Pro Pro Pro	
185 190 195	
cca ccc ccg cag cag cat caa atc cag cat cct tac atg ctc tct cat	677
Pro Pro Pro Gln Gln His Gln Ile Gln His Pro Tyr Met Leu Ser His	
200 205 210	
cag cca tct cct ttt ctc aac atg ggg ggg ctg tat caa gaa gaa gat	725
Gln Pro Ser Pro Phe Leu Asn Met Gly Gly Leu Tyr Gln Glu Glu Asp	
215 220 225 230	
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Gln Met Ala Met Arg Arg Asn Asp Leu Asp Leu Ser Leu Glu Pro Gly	
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 35 40 45

Ser	His	Lys	Gly	Lys	Leu	Phe	Glu	Tyr	Ser	Thr	Asp	Ser	Cys	Met	Glu	
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	65				70					75					80	
Ile	Ala	Pro	Glu	Ser	Asp	Ser	Asn	Thr	Asn	Trp	Ser	Met	Glu	Tyr	Asn	
				85					90					95		
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		115					120						125			
Glu	Gln	Gln	Leu	Asp	Thr	Ala	Leu	Lys	His	Ile	Arg	Ser	Arg	Lys	Asn	
		130				135					140					
Gln	Leu	Met	Tyr	Asp	Ser	Ile	Asn	Glu	Leu	Gln	Arg	Lys	Glu	Lys	Ala	
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Ile	Gln	Glu	Gln	Asn	Ser	Met	Leu	Ser	Lys	Gln	Ile	Lys	Glu	Arg	Glu	
				165					170						175	
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Pro	Tyr	Met	Leu	Ser	His	Gln	Pro	Ser	Pro	Phe	Leu	Asn	Met	Gly	Gly	
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<220>

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Arg	Gln	Val	Thr	Phe	Ser	Lys	Arg	Arg	Ala	Gly	Leu	Met	Lys	Lys	Ala	
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cat	gag	atc	tct	gtt	ctg	tgt	gat	gct	gaa	gtt	gcg	ctt	gtt	gtc	ttc	144
His	Glu	Ile	Ser	Val	Leu	Cys	Asp	Ala	Glu	Val	Ala	Leu	Val	Val	Phe	
		35					40					45				

tcc	cat	aag	ggg	aaa	ctc	ttt	gaa	tac	ccc	act	gat	tct	tgt	atg	gag	192
Ser	His	Lys	Gly	Lys	Leu	Phe	Glu	Tyr	Pro	Thr	Asp	Ser	Cys	Met	Glu	
	50					55					60					

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Glu	Ile	Leu	Glu	Arg	Tyr	Glu	Arg	Tyr	Ser	Tyr	Ala	Glu	Arg	Gln	Leu	
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115 120 125	
gag caa cag ctt gat act gct ctt aag cac atc cgc tct aga aaa aac	432
Glu Gln Gln Leu Asp Thr Ala Leu Lys His Ile Arg Ser Arg Lys Asn	
130 135 140	
caa ctt atg tac gac tcc atc aat gag ctc caa aga aag gag aaa gcc	480
Gln Leu Met Tyr Asp Ser Ile Asn Glu Leu Gln Arg Lys Glu Lys Ala	
145 150 155 160	
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Ile Gln Glu Gln Asn Ser Met Leu Ser Lys Gln Ile Lys Glu Arg Glu	
165 170 175	
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Asn Val Leu Arg Ala Gln Gln Glu Gln Trp Asp Glu Gln Asn His Gly	
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His Asn Met Pro Pro Pro Pro Pro Pro Gln Gln His Gln Ile Gln His	
195 200 205	
cct tac atg ctc tct cat cag cca tct cct ttt ctc aac atg gga ggg	672
Pro Tyr Met Leu Ser His Gln Pro Ser Pro Phe Leu Asn Met Gly Gly	
210 215 220	
ctg tat caa gaa gaa gat caa atg gca atg agg agg aac gat ctc gat	720
Leu Tyr Gln Glu Glu Asp Gln Met Ala Met Arg Arg Asn Asp Leu Asp	
225 230 235 240	
ctg tct ctt gaa ccc gtt tac aac tgc aac ctt ggc cgt cgc tgc tga	768
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35 40 45	

Ser	His	Lys	Gly	Lys	Leu	Phe	Glu	Tyr	Pro	Thr	Asp	Ser	Cys	Met	Glu
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Glu	Ile	Leu	Glu	Arg	Tyr	Glu	Arg	Tyr	Ser	Tyr	Ala	Glu	Arg	Gln	Leu
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Ile	Ala	Pro	Glu	Ser	Asp	Ser	Asn	Thr	Asn	Trp	Ser	Met	Glu	Tyr	Asn
				85					90					95	
Arg	Leu	Lys	Ala	Lys	Ile	Glu	Leu	Leu	Glu	Arg	Asn	Gln	Arg	His	Tyr
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Glu	Gln	Gln	Leu	Asp	Thr	Ala	Leu	Lys	His	Ile	Arg	Ser	Arg	Lys	Asn
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			180					185					190		
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		195					200					205			
Pro	Tyr	Met	Leu	Ser	His	Gln	Pro	Ser	Pro	Phe	Leu	Asn	Met	Gly	Gly
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Leu	Tyr	Gln	Glu	Glu	Asp	Gln	Met	Ala	Met	Arg	Arg	Asn	Asp	Leu	Asp
225					230					235					240
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 Met Gly Arg Gly Lys Val Gln Leu
 1 5
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 Lys Arg Ile Glu Asn Lys Ile Asn Arg Gln Val Thr Phe Ser Lys Arg
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 cgg aac ggc ctg ctc aag aag gcg cac gag atc tcc gtc ctc tgc gat 268
 Arg Asn Gly Leu Leu Lys Lys Ala His Glu Ile Ser Val Leu Cys Asp
 25 30 35 40
 gcc gag gtc gcc gtc atc gtc ttc tcc ccc aag ggc aag ctc tac gag 316
 Ala Glu Val Ala Val Ile Val Phe Ser Pro Lys Gly Lys Leu Tyr Glu
 45 50 55

tac gcc acc gac tcc cgc atg gac aaa att ctt gaa cgc tat gag cga	364
Tyr Ala Thr Asp Ser Arg Met Asp Lys Ile Leu Glu Arg Tyr Glu Arg	
60 65 70	
tat tcc tat gct gaa aag gct ctt att tca gct gaa tct gaa agt gag	412
Tyr Ser Tyr Ala Glu Lys Ala Leu Ile Ser Ala Glu Ser Glu Ser Glu	
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gga aat tgg tgc cac gaa tac agg aaa ctg aag gcc aaa att gag acc	460
Gly Asn Trp Cys His Glu Tyr Arg Lys Leu Lys Ala Lys Ile Glu Thr	
90 95 100	
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Ile Gln Lys Cys His Lys His Leu Met Gly Glu Asp Leu Glu Ser Leu	
105 110 115 120	
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Asn Pro Lys Glu Leu Gln Gln Leu Glu Gln Gln Leu Asp Ser Ser Leu	
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155 160 165	
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Gln Lys Glu Leu Ala Glu Arg Gln Lys Ala Val Ala Ser Arg Gln Gln	
170 175 180	
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Gln Gln Gln Gln Gln Val Gln Trp Asp Gln Gln Thr His Ala Gln Ala	
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Gln Thr Ser Ser Ser Ser Ser Ser Phe Met Met Arg Gln Asp Gln Gln	
205 210 215	
gga ctg ccg cct cca cac aac atc tgc ttc ccg ccg ttg aca atg gga	844
Gly Leu Pro Pro Pro His Asn Ile Cys Phe Pro Pro Leu Thr Met Gly	
220 225 230	
gat aga ggt gaa gag ctg gct gcg gcg gcg gcg gcg cag cag cag cag	892
Asp Arg Gly Glu Glu Leu Ala Ala Ala Ala Ala Ala Gln Gln Gln Gln	
235 240 245	
cca ctg ccg ggg cag gcg caa ccg cag ctc cgc atc gca ggt ctg cca	940
Pro Leu Pro Gly Gln Ala Gln Pro Gln Leu Arg Ile Ala Gly Leu Pro	
250 255 260	
cca tgg atg ctg agc cac ctc aat gca taa ggagagggtc gatgaacaca	990
Pro Trp Met Leu Ser His Leu Asn Ala	
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 35 40 45
 Ser Pro Lys Gly Lys Leu Tyr Glu Tyr Ala Thr Asp Ser Arg Met Asp
 50 55 60
 Lys Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Lys Ala Leu
 65 70 75 80
 Ile Ser Ala Glu Ser Glu Ser Glu Gly Asn Trp Cys His Glu Tyr Arg
 85 90 95
 Lys Leu Lys Ala Lys Ile Glu Thr Ile Gln Lys Cys His Lys His Leu
 100 105 110
 Met Gly Glu Asp Leu Glu Ser Leu Asn Pro Lys Glu Leu Gln Gln Leu
 115 120 125
 Glu Gln Gln Leu Asp Ser Ser Leu Lys His Ile Arg Ser Arg Lys Ser
 130 135 140
 His Leu Met Ala Glu Ser Ile Ser Glu Leu Gln Lys Lys Glu Arg Ser
 145 150 155 160
 Leu Gln Glu Glu Asn Lys Ala Leu Gln Lys Glu Leu Ala Glu Arg Gln
 165 170 175
 Lys Ala Val Ala Ser Arg Gln Gln Gln Gln Gln Gln Val Gln Trp
 180 185 190
 Asp Gln Gln Thr His Ala Gln Ala Gln Thr Ser Ser Ser Ser Ser Ser
 195 200 205
 Phe Met Met Arg Gln Asp Gln Gln Gly Leu Pro Pro Pro His Asn Ile
 210 215 220
 Cys Phe Pro Pro Leu Thr Met Gly Asp Arg Gly Glu Glu Leu Ala Ala
 225 230 235 240
 Ala Ala Ala Ala Gln Gln Gln Gln Pro Leu Pro Gly Gln Ala Gln Pro
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Ile Asn Arg Gln Val Thr Phe Ser Lys Arg Arg Thr Gly Leu Leu Lys
  15              20              25              30

aaa gct cag gag atc tct gtt ctt tgt gat gcc gag gtt tcc ctt att 147
Lys Ala Gln Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ser Leu Ile
          35              40              45

gtc ttc tcc cat aag ggc aaa ttg ttc gag tac tcc tct gaa tct tgc 195
Val Phe Ser His Lys Gly Lys Leu Phe Glu Tyr Ser Ser Glu Ser Cys
          50              55              60

atg gag aag gta cta gaa cgc tac gag agg tat tct tac gcc gag aga 243
Met Glu Lys Val Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Arg
        65              70              75

cag ctg att gca cct gac tct cac gtt aat gca cag acg aac tgg tca 291
Gln Leu Ile Ala Pro Asp Ser His Val Asn Ala Gln Thr Asn Trp Ser
        80              85              90

atg gag tat agc agg ctt aag gcc aag att gag ctt ttg gag aga aac 339
Met Glu Tyr Ser Arg Leu Lys Ala Lys Ile Glu Leu Leu Glu Arg Asn
        95              100             105             110

caa agg cat tat ctg gga gaa gag ttg gaa cca atg agc ctc aag gat 387
Gln Arg His Tyr Leu Gly Glu Glu Leu Gln Pro Met Ser Leu Lys Asp
          115             120             125

ctc caa aat ctg gag cag cag ctt gag act gct ctt aag cac att cgc 435
Leu Gln Asn Leu Glu Gln Gln Leu Glu Thr Ala Leu Lys His Ile Arg
          130             135             140

tcc aga aaa aat caa ctc atg aat gag tcc ctc aac cac ctc caa aga 483
Ser Arg Lys Asn Gln Leu Met Asn Glu Ser Leu Asn His Leu Gln Arg
          145             150             155

aag gag aag gag ata cag gag gaa aac agc atg ctt acc aaa cag ata 531
Lys Glu Lys Glu Ile Gln Glu Glu Asn Ser Met Leu Thr Lys Gln Ile
          160             165             170

aag gag agg gaa aac atc cta aag aca aaa caa acc caa tgt gag cag 579
Lys Glu Arg Glu Asn Ile Leu Lys Thr Lys Gln Thr Gln Cys Glu Gln
          175             180             185             190

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ctg aac cgc agc gtc gac gat gta cca cag cca caa cca ttt caa cac 627
 Leu Asn Arg Ser Val Asp Asp Val Pro Gln Pro Gln Pro Phe Gln His
 195 200 205

ccc cat ctt tac atg atc gct cat cag act tct cct ttc cta aat atg 675
 Pro His Leu Tyr Met Ile Ala His Gln Thr Ser Pro Phe Leu Asn Met
 210 215 220

ggt ggt ttg tac caa gga gaa gac caa acg gcg atg agg agg aac aat 723
 Gly Gly Leu Tyr Gln Gly Glu Asp Gln Thr Ala Met Arg Arg Asn Asn
 225 230 235

ctg gat ctg act ctt gaa ccc att tac aat tac ctt ggc tgt tac gcc 771
 Leu Asp Leu Thr Leu Glu Pro Ile Tyr Asn Tyr Leu Gly Cys Tyr Ala
 240 245 250

gct tga nn 779
 Ala
 255

<210> 10
 <211> 255
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> CAULIFLOWER (CAL)

<400> 10
 Met Gly Arg Gly Arg Val Glu Leu Lys Arg Ile Glu Asn Lys Ile Asn
 1 5 10 15
 Arg Gln Val Thr Phe Ser Lys Arg Arg Thr Gly Leu Leu Lys Lys Ala
 20 25 30
 Gln Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ser Leu Ile Val Phe
 35 40 45
 Ser His Lys Gly Lys Leu Phe Glu Tyr Ser Ser Glu Ser Cys Met Glu
 50 55 60
 Lys Val Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Arg Gln Leu
 65 70 75 80
 Ile Ala Pro Asp Ser His Val Asn Ala Gln Thr Asn Trp Ser Met Glu
 85 90 95
 Tyr Ser Arg Leu Lys Ala Lys Ile Glu Leu Leu Glu Arg Asn Gln Arg
 100 105 110
 His Tyr Leu Gly Glu Glu Leu Glu Pro Met Ser Leu Lys Asp Leu Gln
 115 120 125
 Asn Leu Glu Gln Gln Leu Glu Thr Ala Leu Lys His Ile Arg Ser Arg
 130 135 140
 Lys Asn Gln Leu Met Asn Glu Ser Leu Asn His Leu Gln Arg Lys Glu
 145 150 155 160
 Lys Glu Ile Gln Glu Glu Asn Ser Met Leu Thr Lys Gln Ile Lys Glu
 165 170 175
 Arg Glu Asn Ile Leu Lys Thr Lys Gln Thr Gln Cys Glu Gln Leu Asn
 180 185 190
 Arg Ser Val Asp Asp Val Pro Gln Pro Gln Pro Phe Gln His Pro His
 195 200 205
 Leu Tyr Met Ile Ala His Gln Thr Ser Pro Phe Leu Asn Met Gly Gly
 210 215 220
 Leu Tyr Gln Gly Glu Asp Gln Thr Ala Met Arg Arg Asn Asn Leu Asp
 225 230 235 240

Leu Thr Leu Glu Pro Ile Tyr Asn Tyr Leu Gly Cys Tyr Ala Ala
245 250 255

<210> 11
<211> 756
<212> DNA
<213> Brassica oleracea

<220>
<221> CDS
<222> (1)..(756)
<223> CAULIFLOWER

<400> 11
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Met Gly Arg Gly Arg Val Glu Met Lys Arg Ile Glu Asn Lys Ile Asn
1 5 10 15
cga caa gtg acg ttt tcg aaa aga aga gct ggt ctt ttg aag aaa gcc 96
Arg Gln Val Thr Phe Ser Lys Arg Arg Ala Gly Leu Leu Lys Lys Ala
20 25 30
cat gag atc tcg atc ctt tgt gat gct gag gtt tcc ctt att gtc ttc 144
His Glu Ile Ser Ile Leu Cys Asp Ala Glu Val Ser Leu Ile Val Phe
35 40 45
tcc cat aag ggg aaa ctg ttc gag tac tcg tct gaa tct tgc atg gag 192
Ser His Lys Gly Lys Leu Phe Glu Tyr Ser Ser Glu Ser Cys Met Glu
50 55 60
aag gta cta gaa cac tac gag agg tac tct tac gcc gag aaa cag cta 240
Lys Val Leu Glu His Tyr Glu Arg Tyr Ser Tyr Ala Glu Lys Gln Leu
65 70 75 80
aaa gtt cca gac tct cac gtc aat gca caa acg aac tgg tca gtg gaa 288
Lys Val Pro Asp Ser His Val Asn Ala Gln Thr Asn Trp Ser Val Glu
85 90 95
tat agc agg ctt aag gct aag att gag ctt ttg gag aga aac caa agg 336
Tyr Ser Arg Leu Lys Ala Lys Ile Glu Leu Leu Glu Arg Asn Gln Arg
100 105 110
cat tat ctg ggc gaa gat tta gaa tca atc agc ata aag gag cta cag 384
His Tyr Leu Gly Glu Asp Leu Glu Ser Ile Ser Ile Lys Glu Leu Gln
115 120 125
aat ctg gag cag cag ctt gac act tct ctt aaa cat att cgc tcg aga 432
Asn Leu Glu Gln Gln Leu Asp Thr Ser Leu Lys His Ile Arg Ser Arg
130 135 140
aaa aat caa cta atg cac gag tcc ctc aac cac ctc caa aga aag gag 480
Lys Asn Gln Leu Met His Glu Ser Leu Asn His Leu Gln Arg Lys Glu
145 150 155 160
aaa gaa ata ctg gag gaa aac agc atg ctt gcc aaa cag ata agg gag 528
Lys Glu Ile Leu Glu Glu Asn Ser Met Leu Ala Lys Gln Ile Arg Glu
165 170 175

agg gag agt atc cta agg aca cat caa aac caa tca gag cag caa aac 576
 Arg Glu Ser Ile Leu Arg Thr His Gln Asn Gln Ser Glu Gln Gln Asn
 180 185 190

cgc agc cac cat gta gct cct cag ccg caa ccg cag tta aat cct tac 624
 Arg Ser His His Val Ala Pro Gln Pro Gln Pro Gln Leu Asn Pro Tyr
 195 200 205

atg gca tca tct cct ttc cta aat atg ggt ggc atg tac caa gga gaa 672
 Met Ala Ser Ser Pro Phe Leu Asn Met Gly Gly Met Tyr Gln Gly Glu
 210 215 220

tat cca acg gcg gtg agg agg aac cgt ctc gat ctg act ctt gaa ccc 720
 Tyr Pro Thr Ala Val Arg Arg Asn Arg Leu Asp Leu Thr Leu Glu Pro
 225 230 235 240

att tac aac tgc aac ctt ggt tac ttt gcc gca tga 756
 Ile Tyr Asn Cys Asn Leu Gly Tyr Phe Ala Ala
 245 250

<210> 12
 <211> 251
 <212> PRT
 <213> Brassica oleracea

<220>
 <223> CAULIFLOWER (CAL)

<400> 12
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 Arg Gln Val Thr Phe Ser Lys Arg Arg Ala Gly Leu Leu Lys Lys Ala
 20 25 30
 His Glu Ile Ser Ile Leu Cys Asp Ala Glu Val Ser Leu Ile Val Phe
 35 40 45
 Ser His Lys Gly Lys Leu Phe Glu Tyr Ser Ser Glu Ser Cys Met Glu
 50 55 60
 Lys Val Leu Glu His Tyr Glu Arg Tyr Ser Tyr Ala Glu Lys Gln Leu
 65 70 75 80
 Lys Val Pro Asp Ser His Val Asn Ala Gln Thr Asn Trp Ser Val Glu
 85 90 95
 Tyr Ser Arg Leu Lys Ala Lys Ile Glu Leu Leu Glu Arg Asn Gln Arg
 100 105 110
 His Tyr Leu Gly Glu Asp Leu Glu Ser Ile Ser Ile Lys Glu Leu Gln
 115 120 125
 Asn Leu Glu Gln Gln Leu Asp Thr Ser Leu Lys His Ile Arg Ser Arg
 130 135 140
 Lys Asn Gln Leu Met His Glu Ser Leu Asn His Leu Gln Arg Lys Glu
 145 150 155 160
 Lys Glu Ile Leu Glu Asn Ser Met Leu Ala Lys Gln Ile Arg Glu
 165 170 175
 Arg Glu Ser Ile Leu Arg Thr His Gln Asn Gln Ser Glu Gln Gln Asn
 180 185 190
 Arg Ser His His Val Ala Pro Gln Pro Gln Pro Gln Leu Asn Pro Tyr
 195 200 205
 Met Ala Ser Ser Pro Phe Leu Asn Met Gly Gly Met Tyr Gln Gly Glu
 210 215 220
 Tyr Pro Thr Ala Val Arg Arg Asn Arg Leu Asp Leu Thr Leu Glu Pro
 225 230 235 240

Ile Tyr Asn Cys Asn Leu Gly Tyr Phe Ala Ala
 245 250

<210> 13
 <211> 756
 <212> DNA
 <213> Brassica oleracea var. botrytis

<220>
 <221> CDS
 <222> (1) .. (453)
 <223> CAULIFLOWER

<400> 13
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 Met Gly Arg Gly Arg Val Glu Met Lys Arg Ile Glu Asn Lys Ile Asn
 1 5 10 15
 aga caa gtg acg ttt tcg aaa aga aga gct ggt ctt ttg aag aaa gcc 96
 Arg Gln Val Thr Phe Ser Lys Arg Arg Ala Gly Leu Leu Lys Lys Ala
 20 25 30
 cat gag atc tcg att ctt tgt gat gct gag gtt tcc ctt att gtc ttc 144
 His Glu Ile Ser Ile Leu Cys Asp Ala Glu Val Ser Leu Ile Val Phe
 35 40 45
 tcc cat aag ggg aaa ctg ttc gag tac tcg tct gaa tct tgc atg gag 192
 Ser His Lys Gly Lys Leu Phe Glu Tyr Ser Ser Glu Ser Cys Met Glu
 50 55 60
 aag gta cta gaa cgc tac gag agg tac tct tac gcc gag aaa cag cta 240
 Lys Val Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Lys Gln Leu
 65 70 75 80
 aaa gct cca gac tct cac gtc aat gca caa acg aac tgg tca atg gaa 288
 Lys Ala Pro Asp Ser His Val Asn Ala Gln Thr Asn Trp Ser Met Glu
 85 90 95
 tat agc agg ctt aag gct aag att gag ctt tgg gag agg aac caa agg 336
 Tyr Ser Arg Leu Lys Ala Lys Ile Glu Leu Trp Glu Arg Asn Gln Arg
 100 105 110
 cat tat ctg gga gaa gat tta gaa tca atc agc ata aag gag cta cag 384
 His Tyr Leu Gly Glu Asp Leu Glu Ser Ile Ser Ile Lys Glu Leu Gln
 115 120 125
 aat ctg gag cag cag ctt gac act tct ctt aaa cat att cgc tcc aga 432
 Asn Leu Glu Gln Gln Leu Asp Thr Ser Leu Lys His Ile Arg Ser Arg
 130 135 140
 aaa aat caa cta atg cac tag tccctcaacc acctccaaag aaaggagaaa 483
 Lys Asn Gln Leu Met His
 145 150
 gaaatactgg aggaaaacag catgcttgcc aaacagataa aggagagggga gagtatccta 543
 aggacacatc aaaaccaatc agagcagcaa aaccgcagcc accatgtagc tcctcagccg 603
 caaccgcagt taaatcctta catggcatca tctcctttcc taaatatggg tggcatgtac 663

caaggagaat atccaacggc ggtgaggagg aaccgtctcg atctgactct tgaacccatt 723

tacaactgca accttggtta ctttgccgca tga

756

<210> 14

<211> 150

<212> PRT

<213> Brassica oleracea var. botrytis

<220>

<223> CAULIFLOWER (CAL)

<400> 14

Met	Gly	Arg	Gly	Arg	Val	Glu	Met	Lys	Arg	Ile	Glu	Asn	Lys	Ile	Asn
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Arg	Gln	Val	Thr	Phe	Ser	Lys	Arg	Arg	Ala	Gly	Leu	Leu	Lys	Lys	Ala
			20					25					30		
His	Glu	Ile	Ser	Ile	Leu	Cys	Asp	Ala	Glu	Val	Ser	Leu	Ile	Val	Phe
		35					40					45			
Ser	His	Lys	Gly	Lys	Leu	Phe	Glu	Tyr	Ser	Ser	Glu	Ser	Cys	Met	Glu
	50					55					60				
Lys	Val	Leu	Glu	Arg	Tyr	Glu	Arg	Tyr	Ser	Tyr	Ala	Glu	Lys	Gln	Leu
65					70					75					80
Lys	Ala	Pro	Asp	Ser	His	Val	Asn	Ala	Gln	Thr	Asn	Trp	Ser	Met	Glu
				85					90					95	
Tyr	Ser	Arg	Leu	Lys	Ala	Lys	Ile	Glu	Leu	Trp	Glu	Arg	Asn	Gln	Arg
			100					105					110		
His	Tyr	Leu	Gly	Glu	Asp	Leu	Glu	Ser	Ile	Ser	Ile	Lys	Glu	Leu	Gln
		115					120					125			
Asn	Leu	Glu	Gln	Gln	Leu	Asp	Thr	Ser	Leu	Lys	His	Ile	Arg	Ser	Arg
	130					135						140			
Lys	Asn	Gln	Leu	Met	His										
145					150										

<210> 15

<211> 1500

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (72)..(1346)

<223> LEAFY (LFY)

<400> 15

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aaaaatagat	t atg gat cct gaa ggt ttc acg agt ggc tta ttc cgg tgg	110				
	Met Asp Pro Glu Gly Phe Thr Ser Gly Leu Phe Arg Trp					
	1 5 10					
aac cca acg aga gca ttg gtt caa gca cca cct ccg gtt cca cct ccg	158					
Asn Pro Thr Arg Ala Leu Val Gln Ala Pro Pro Pro Val Pro Pro Pro						
15 20 25						
ctg cag caa cag ccg gtg aca ccg cag acg gct gct ttt ggg atg cga	206					
Leu Gln Gln Gln Pro Val Thr Pro Gln Thr Ala Ala Phe Gly Met Arg						
30 35 40 45						

ctt ggt ggt tta gag gga cta ttc ggt cca tac ggt ata cgt ttc tac	254
Leu Gly Gly Leu Glu Gly Leu Phe Gly Pro Tyr Gly Ile Arg Phe Tyr	
50 55 60	
acg gcg gcg aag ata gcg gag tta ggt ttt acg gcg agc acg ctt gtg	302
Thr Ala Ala Lys Ile Ala Glu Leu Gly Phe Thr Ala Ser Thr Leu Val	
65 70 75	
ggt atg aag gac gag gag ctt gaa gag atg atg aat agt ctc tct cat	350
Gly Met Lys Asp Glu Glu Leu Glu Glu Met Met Asn Ser Leu Ser His	
80 85 90	
atc ttt cgt tgg gag ctt ctt gtt ggt gaa cgg tac ggt atc aaa gct	398
Ile Phe Arg Trp Glu Leu Leu Val Gly Glu Arg Tyr Gly Ile Lys Ala	
95 100 105	
gcc gtt aga gct gaa cgg aga cga ttg caa gaa gag gag gaa gag gaa	446
Ala Val Arg Ala Glu Arg Arg Arg Leu Gln Glu Glu Glu Glu Glu	
110 115 120 125	
tct tct aga cgc cgt cat ttg cta ctc tcc gcc gct ggt gat tcc ggt	494
Ser Ser Arg Arg Arg His Leu Leu Leu Ser Ala Ala Gly Asp Ser Gly	
130 135 140	
act cat cac gct ctt gat gct ctc tcc caa gaa gat gat tgg aca ggg	542
Thr His His Ala Leu Asp Ala Leu Ser Gln Glu Asp Asp Trp Thr Gly	
145 150 155	
tta tct gag gaa ccg gtg cag caa caa gac cag act gat gcg gcg ggg	590
Leu Ser Glu Glu Pro Val Gln Gln Gln Asp Gln Thr Asp Ala Ala Gly	
160 165 170	
aat aac ggc gga gga gga agt ggt tac tgg gac gca ggt caa gga aag	638
Asn Asn Gly Gly Gly Gly Ser Gly Tyr Trp Asp Ala Gly Gln Gly Lys	
175 180 185	
atg aag aag caa cag cag cag aga cgg aga aag aaa cca atg ctg acg	686
Met Lys Lys Gln Gln Gln Gln Arg Arg Arg Lys Lys Pro Met Leu Thr	
190 195 200 205	
tca gtg gaa acc gac gaa gac gtc aac gaa ggt gag gat gac gac ggg	734
Ser Val Glu Thr Asp Glu Asp Val Asn Glu Gly Glu Asp Asp Asp Gly	
210 215 220	
atg gat aac ggc aac gga ggt agt ggt ttg ggg aca gag aga cag agg	782
Met Asp Asn Gly Asn Gly Gly Ser Gly Leu Gly Thr Glu Arg Gln Arg	
225 230 235	
gag cat ccg ttt atc gta acg gag cct ggg gaa gtg gca cgt ggc aaa	830
Glu His Pro Phe Ile Val Thr Glu Pro Gly Glu Val Ala Arg Gly Lys	
240 245 250	
aag aac ggc tta gat tat ctg ttc cac ttg tac gaa caa tgc cgt gag	878
Lys Asn Gly Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln Cys Arg Glu	
255 260 265	
ttc ctt ctt cag gtc cag aca att gct aaa gac cgt ggc gaa aaa tgc	926
Phe Leu Leu Gln Val Gln Thr Ile Ala Lys Asp Arg Gly Glu Lys Cys	
270 275 280 285	

ccc acc aag gtg acg aac caa gta ttc agg tac gcg aag aaa tca gga 974
 Pro Thr Lys Val Thr Asn Gln Val Phe Arg Tyr Ala Lys Lys Ser Gly
 290 295 300

gcg agt tac ata aac aag cct aaa atg cga cac tac gtt cac tgt tac 1022
 Ala Ser Tyr Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr
 305 310 315

gct ctc cac tgc cta gac gaa gaa gct tca aat gct ctc aga aga gcg 1070
 Ala Leu His Cys Leu Asp Glu Glu Ala Ser Asn Ala Leu Arg Arg Ala
 320 325 330

ttt aaa gaa cgc ggt gag aac gtt ggc tca tgg cgt cag gct tgt tac 1118
 Phe Lys Glu Arg Gly Glu Asn Val Gly Ser Trp Arg Gln Ala Cys Tyr
 335 340 345

aag cca ctt gtg aac atc gct tgt cgt cat ggc tgg gat ata gac gcc 1166
 Lys Pro Leu Val Asn Ile Ala Cys Arg His Gly Trp Asp Ile Asp Ala
 350 355 360 365

gtc ttt aac gct cat cct cgt ctc tct att tgg tat gtt cca aca aag 1214
 Val Phe Asn Ala His Pro Arg Leu Ser Ile Trp Tyr Val Pro Thr Lys
 370 375 380

ctg cgt cag ctt tgc cat ttg gag cgg aac aat gcg gtt gct gcg gct 1262
 Leu Arg Gln Leu Cys His Leu Glu Arg Asn Asn Ala Val Ala Ala Ala
 385 390 395

gcg gct tta gtt ggc ggt att agc tgt acc gga tcg tcg acg tct gga 1310
 Ala Ala Leu Val Gly Gly Ile Ser Cys Thr Gly Ser Ser Thr Ser Gly
 400 405 410

cgt ggt gga tgc ggc ggc gac gac ttg cgt ttc tag tttggtttgg 1356
 Arg Gly Gly Cys Gly Gly Asp Asp Leu Arg Phe
 415 420 425

gtagttgtgg tttgttttagt cgttatccta attaaactatt agtctttaat ttagtcttct 1416

tggctaattt atttttcttt ttttgtcaaa acctttaatt tggtatggct aatttggtat 1476

acacgcagtt ttcttaatgc gtta 1500

<210> 16
 <211> 424
 <212> PRT
 <213> *Arabidopsis thaliana*

<220>
 <223> LEAFY (LFY)

<400> 16
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 1 5 10 15
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 20 25 30
 Gln Pro Val Thr Pro Gln Thr Ala Ala Phe Gly Met Arg Leu Gly Gly
 35 40 45
 Leu Glu Gly Leu Phe Gly Pro Tyr Gly Ile Arg Phe Tyr Thr Ala Ala
 50 55 60

Lys Ile Ala Glu Leu Gly Phe Thr Ala Ser Thr Leu Val Gly Met Lys
 65 70 75 80
 Asp Glu Glu Leu Glu Glu Met Met Asn Ser Leu Ser His Ile Phe Arg
 85 90 95
 Trp Glu Leu Leu Val Gly Glu Arg Tyr Gly Ile Lys Ala Ala Val Arg
 100 105 110
 Ala Glu Arg Arg Arg Leu Gln Glu Glu Glu Glu Ser Ser Arg
 115 120 125
 Arg Arg His Leu Leu Leu Ser Ala Ala Gly Asp Ser Gly Thr His His
 130 135 140
 Ala Leu Asp Ala Leu Ser Gln Glu Asp Asp Trp Thr Gly Leu Ser Glu
 145 150 155 160
 Glu Pro Val Gln Gln Asp Gln Thr Asp Ala Ala Gly Asn Asn Gly
 165 170 175
 Gly Gly Gly Ser Gly Tyr Trp Asp Ala Gly Gln Gly Lys Met Lys Lys
 180 185 190
 Gln Gln Gln Gln Arg Arg Arg Lys Pro Met Leu Thr Ser Val Glu
 195 200 205
 Thr Asp Glu Asp Val Asn Glu Gly Glu Asp Asp Asp Gly Met Asp Asn
 210 215 220
 Gly Asn Gly Gly Ser Gly Leu Gly Thr Glu Arg Gln Arg Glu His Pro
 225 230 235 240
 Phe Ile Val Thr Glu Pro Gly Glu Val Ala Arg Gly Lys Lys Asn Gly
 245 250 255
 Leu Asp Tyr Leu Phe His Leu Tyr Glu Gln Cys Arg Glu Phe Leu Leu
 260 265 270
 Gln Val Gln Thr Ile Ala Lys Asp Arg Gly Glu Lys Cys Pro Thr Lys
 275 280 285
 Val Thr Asn Gln Val Phe Arg Tyr Ala Lys Lys Ser Gly Ala Ser Tyr
 290 295 300
 Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu His
 305 310 315 320
 Cys Leu Asp Glu Glu Ala Ser Asn Ala Leu Arg Arg Ala Phe Lys Glu
 325 330 335
 Arg Gly Glu Asn Val Gly Ser Trp Arg Gln Ala Cys Tyr Lys Pro Leu
 340 345 350
 Val Asn Ile Ala Cys Arg His Gly Trp Asp Ile Asp Ala Val Phe Asn
 355 360 365
 Ala His Pro Arg Leu Ser Ile Trp Tyr Val Pro Thr Lys Leu Arg Gln
 370 375 380
 Leu Cys His Leu Glu Arg Asn Asn Ala Val Ala Ala Ala Ala Leu
 385 390 395 400
 Val Gly Gly Ile Ser Cys Thr Gly Ser Ser Thr Ser Gly Arg Gly Gly
 405 410 415
 Cys Gly Gly Asp Asp Leu Arg Phe
 420

<210> 17
 <211> 1656
 <212> DNA
 <213> *Drosophila melanogaster*

 <220>
 <221> CDS
 <222> (1)..(1653)
 <223> ecdysone receptor ligand binding domain

<400> 17

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cgc gaa aag aag gcc cag aag gag aag gac aaa atg acc act tcg ccg	96
Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro	
20 25 30	
agc tct cag cat gcc gcc aat gcc agc ttg gcc tct ggt gcc gcc caa	144
Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln	
35 40 45	
gac ttt gtt aag aag gag att ctt gac ctt atg aca tgc gag ccg ccc	192
Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro	
50 55 60	
cag cat gcc act att ccg cta cta cct gat gaa ata ttg gcc aag tgt	240
Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys	
65 70 75 80	
caa gcg cgc aat ata cct tcc tta acg tac aat cag ttg gcc gtt ata	288
Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile	
85 90 95	
tac aag tta att tgg tac cag gat gcc tat gag cag cca tct gaa gag	336
Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu	
100 105 110	
gat ctc agg cgt ata atg agt caa ccc gat gag aac gag agc caa acg	384
Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr	
115 120 125	
gac gtc agc ttt ccg cat ata acc gag ata acc ata ctc acg gtc cag	432
Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln	
130 135 140	
ttg att gtt gag ttt gct aaa ggt cta cca gcg ttt aca aag ata ccc	480
Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro	
145 150 155 160	
cag gag gac cag atc acg tta cta aag gcc tgc tcg tcg gag gtg atg	528
Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met	
165 170 175	
atg ctg cgt atg gca cga cgc tat gac cac agc tcg gac tca ata ttc	576
Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe	
180 185 190	
ttc gcg aat aat aga tca tat acg ccg gat tct tac aaa atg gcc gga	624
Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly	
195 200 205	
atg gct gat aac att gaa gac ctg ctg cat ttc tgc cgc caa atg ttc	672
Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe	
210 215 220	
tcg atg aag gtg gac aac gtc gaa tac gcg ctt ctc act gcc att gtg	720
Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val	
225 230 235 240	

atc ttc tcg gac cgg ccg ggc ctg gag aag gcc caa cta gtc gaa gcg	768
Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala	
245 250 255	
atc cag agc tac tac atc gac acg cta cgc att tat ata ctc aac cgc	816
Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg	
260 265 270	
cac tgc ggc gac tca atg agc ctc gtc ttc tac gca aag ctg ctc tcg	864
His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser	
275 280 285	
atc ctc acc gag ctg cgt acg ctg ggc aac cag aac gcc gag atg tgt	912
Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys	
290 295 300	
ttc tca cta aag ctc aaa aac cgc aaa ctg ccc aag ttc ctc gag gag	960
Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu	
305 310 315 320	
atc tgg gac gtt cat gcc atc ccg cca tcg gtc cag tcg cac ctt cag	1008
Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln	
325 330 335	
att acc cag gag gag aac gag cgt ctc gag cgg gct gag cgt atg cgg	1056
Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg	
340 345 350	
gca tcg gtt ggg ggc gcc att acc gcc ggc att gat tgc gac tct gcc	1104
Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala	
355 360 365	
tcc act tcg gcg gcg gca gcc gcg gcc cag cat cag cct cag cct cag	1152
Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln	
370 375 380	
ccc cag ccc caa ccc tcc tcc ctg acc cag aac gat tcc cag cac cag	1200
Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln	
385 390 395 400	
aca cag ccg cag cta caa cct cag cta cca cct cag ctg caa ggt caa	1248
Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln	
405 410 415	
ctg caa ccc cag ctc caa cca cag ctt cag acg caa ctc cag cca cag	1296
Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln	
420 425 430	
att caa cca cag cca cag ctc ctt ccc gtc tcc gct ccc gtg ccc gcc	1344
Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala	
435 440 445	
tcc gta acc gca cct ggt tcc ttg tcc gcg gtc agt acg agc agc gaa	1392
Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu	
450 455 460	
tac atg ggc gga agt gcg gcc ata gga ccc atc acg ccg gca acc acc	1440
Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr	
465 470 475 480	

agc agt atc acg gct gcc gtt acc gct agc tcc acc aca tca gcg gta 1488
 Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val
 485 490 495
 ccg atg ggc aac gga gtt gga gtc ggt gtt ggg gtg ggc ggc aac gtc 1536
 Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val Gly Val Gly Asn Val
 500 505 510
 agc atg tat gcg aac gcc cag acg gcg atg gcc ttg atg ggt gta gcc 1584
 Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala
 515 520 525
 ctg cat tcg cac caa gag cag ctt atc ggg gga gtg gcg gtt aag tcg 1632
 Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser
 530 535 540
 gag cac tcg acg act gca tag cag 1656
 Glu His Ser Thr Thr Ala
 545 550

<210> 18
 <211> 550
 <212> PRT
 <213> Drosophila melanogaster

<220>
 <223> ecdysone receptor ligand binding domain

<400> 18
 Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg
 1 5 10 15
 Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro
 20 25 30
 Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln
 35 40 45
 Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro
 50 55 60
 Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys
 65 70 75 80
 Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile
 85 90 95
 Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu
 100 105 110
 Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr
 115 120 125
 Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln
 130 135 140
 Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro
 145 150 155 160
 Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met
 165 170 175
 Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe
 180 185 190
 Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly
 195 200 205
 Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe
 210 215 220
 Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val
 225 230 235 240

Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala
 245 250 255
 Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg
 260 265 270
 His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser
 275 280 285
 Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys
 290 295 300
 Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu
 305 310 315 320
 Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln
 325 330 335
 Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg
 340 345 350
 Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala
 355 360 365
 Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln
 370 375 380
 Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln
 385 390 395 400
 Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln
 405 410 415
 Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln
 420 425 430
 Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala
 435 440 445
 Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu
 450 455 460
 Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr
 465 470 475 480
 Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val
 485 490 495
 Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Gly Asn Val
 500 505 510
 Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala
 515 520 525
 Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser
 530 535 540
 Glu His Ser Thr Thr Ala
 545 550

<210> 19

<211> 855

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(855)

<223> rat glucocorticoid receptor ligand binding domain

<400> 19

aca aag aaa aaa atc aaa ggg att cag caa gcc act gca gga gtc tca 48
 Thr Lys Lys Lys Ile Lys Gly Ile Gln Gln Ala Thr Ala Gly Val Ser
 1 5 10 15
 caa gac act tcg gaa aat cct aac aaa aca ata gtt cct gca gca tta 96
 Gln Asp Thr Ser Glu Asn Pro Asn Lys Thr Ile Val Pro Ala Ala Leu
 20 25 30

cca cag ctc acc cct acc ttg gtg tca ctg ctg gag gtg att gaa ccc	144
Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro	
35 40 45	
gag gtg ttg tat gca gga tat gat agc tct gtt cca gat tca gca tgg	192
Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Ala Trp	
50 55 60	
aga att atg acc aca ctc aac atg tta ggt ggg cgt caa gtg att gca	240
Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala	
65 70 75 80	
gca gtg aaa tgg gca aag gcg ata cta ggc ttg aga aac tta cac ctc	288
Ala Val Lys Trp Ala Lys Ala Ile Leu Gly Leu Arg Asn Leu His Leu	
85 90 95	
gat gac caa atg acc ctg cta cag tac tca tgg atg ttt ctc atg gca	336
Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala	
100 105 110	
ttt gcc ttg ggt tgg aga tca tac aga caa tca agc gga aac ctg ctc	384
Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser Ser Gly Asn Leu Leu	
115 120 125	
tgc ttt gct cct gat ctg att att aat gag cag aga atg tct cta ccc	432
Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Ser Leu Pro	
130 135 140	
tgc atg tat gac caa tgt aaa cac atg ctg ttt gtc tcc tct gaa tta	480
Cys Met Tyr Asp Gln Cys Lys His Met Leu Phe Val Ser Ser Glu Leu	
145 150 155 160	
caa aga ttg cag gta tcc tat gaa gag tat ctc tgt atg aaa acc tta	528
Gln Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu	
165 170 175	
ctg ctt ctc tcc tca gtt gct aag gaa ggt ctg aag agc caa gag tta	576
Leu Leu Leu Ser Ser Val Ala Lys Glu Gly Leu Lys Ser Gln Glu Leu	
180 185 190	
ttt gat gag att cga atg act tat atc aaa gag cta gga aaa gcc atc	624
Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile	
195 200 205	
gtc aaa agg gaa ggg aac tcc agt cag aac tgg caa cgg ttt tac caa	672
Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln	
210 215 220	
ctg aca aag ctt ctg gac tcc atg cat gag gtg gtt gag aat ctc ctt	720
Leu Thr Lys Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu	
225 230 235 240	
acc tac tgc ttc cag aca ttt ttg gat aag acc atg agt att gaa ttc	768
Thr Tyr Cys Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe	
245 250 255	
cca gag atg tta gct gaa atc atc act aat cag ata cca aaa tat tca	816
Pro Glu Met Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser	
260 265 270	

aat gga aat atc aaa aag ctt ctg ttt cat caa aaa tga
 Asn Gly Asn Ile Lys Lys Leu Leu Phe His Gln Lys
 275 280 285

855

<210> 20
 <211> 284
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> rat glucocorticoid receptor ligand binding domain

<400> 20
 Thr Lys Lys Lys Ile Lys Gly Ile Gln Gln Ala Thr Ala Gly Val Ser
 1 5 10 15
 Gln Asp Thr Ser Glu Asn Pro Asn Lys Thr Ile Val Pro Ala Ala Leu
 20 25 30
 Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro
 35 40 45
 Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Ala Trp
 50 55 60
 Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala
 65 70 75 80
 Ala Val Lys Trp Ala Lys Ala Ile Leu Gly Leu Arg Asn Leu His Leu
 85 90 95
 Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala
 100 105 110
 Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser Ser Gly Asn Leu Leu
 115 120 125
 Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Ser Leu Pro
 130 135 140
 Cys Met Tyr Asp Gln Cys Lys His Met Leu Phe Val Ser Ser Glu Leu
 145 150 155 160
 Gln Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu
 165 170 175
 Leu Leu Leu Ser Ser Val Ala Lys Glu Gly Leu Lys Ser Gln Glu Leu
 180 185 190
 Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile
 195 200 205
 Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln
 210 215 220
 Leu Thr Lys Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu
 225 230 235 240
 Thr Tyr Cys Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe
 245 250 255
 Pro Glu Met Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser
 260 265 270
 Asn Gly Asn Ile Lys Lys Leu Leu Phe His Gln Lys
 275 280

<210> 21
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:copper
 inducible regulatory element, ACE1 binding site
 from metallothionein gene promoter

<400> 21
agcttagcga tgcgtctttt ccgctgaacc gttccagcaa aaaagactag 50

<210> 22
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:tet operator
sequence

<400> 22
actctatcag tgatagagt 19

<210> 23
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ecdysone
response element (EcRE)

<400> 23
gatccgacaa ggggttcaatg cacttgta 29

<210> 24
<211> 371
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> inducible regulatory element from HSP81-1 heat
shock gene promoter

<400> 24
gtggagtctc gaaacgaaaa gaactttctg gaattcggtt gtcacaaaag ctaaaaacgg 60
ttgatttcat cgaaatacgg cgtcgttttc aaagaacaat ccagaaatca ctggttttcc 120
tttatttcaa aagaagagac tagaacttta tttctcctct ataaaatcac tttgtttttc 180
cctctcttct tcataaatca acaaaacaat cacaaatctc tcgaaacgct ctcgaaagttc 240
caaattttct cttagcattc ttttctggtt ctggtttgcg ttgaatcaaa gttcgttgcg 300
atggcggtatg ttcagatggc tgatgcagag acttttggtt tccaagctga gattaaccag 360
cttcttagct t 371

<210> 25

<400> 25
000

<210> 26

<400> 26
000

<210> 27
 <211> 747
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(747)
 <223> SEPALLATA1 (SEP1)

<400> 27
 atg gga aga gga aga gta gag ctg aag agg ata gag aac aaa atc aac 48
 Met Gly Arg Gly Arg Val Glu Leu Lys Arg Ile Glu Asn Lys Ile Asn
 1 5 10 15
 aga caa gta acg ttt gca aag cgt agg aac ggt ttg ttg aag aaa gct 96
 Arg Gln Val Thr Phe Ala Lys Arg Asn Gly Leu Leu Lys Lys Ala
 20 25 30
 tat gaa ttg tct gtt ctc tgt gat gct gaa gtt gct ctc atc atc ttc 144
 Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Ile Phe
 35 40 45
 tcc aac cgt gga aag ctc tat gag ttt tgc agc tcc tca aac atg ctc 192
 Ser Asn Arg Gly Lys Leu Tyr Glu Phe Cys Ser Ser Ser Asn Met Leu
 50 55 60
 aag aca ctt gat cgg tac cag aaa tgc agc tat gga tcc att gaa gtc 240
 Lys Thr Leu Asp Arg Tyr Gln Lys Cys Ser Tyr Gly Ser Ile Glu Val
 65 70 75 80
 aac aac aaa cct gcc aaa gaa ctt gag aac agc tac aga gaa tat ctg 288
 Asn Asn Lys Pro Ala Lys Glu Leu Glu Asn Ser Tyr Arg Glu Tyr Leu
 85 90 95
 aag ctt aag ggt aga tat gag aac ctt caa cgt caa cag aga aat ctt 336
 Lys Leu Lys Gly Arg Tyr Glu Asn Leu Gln Arg Gln Gln Arg Asn Leu
 100 105 110
 ctt ggg gag gat tta gga cct ttg aat tca aag gag tta gag cag ctt 384
 Leu Gly Glu Asp Leu Gly Pro Leu Asn Ser Lys Glu Leu Glu Gln Leu
 115 120 125
 gag cgt caa ctg gac ggc tct ctc aag caa gtt cgg tcc atc aag aca 432
 Glu Arg Gln Leu Asp Gly Ser Leu Lys Gln Val Arg Ser Ile Lys Thr
 130 135 140
 cag tac atg ctt gac cag ctc tcg gat ctt caa aat aaa gag caa atg 480
 Gln Tyr Met Leu Asp Gln Leu Ser Asp Leu Gln Asn Lys Glu Gln Met
 145 150 155 160
 ttg ctt gaa acc aat aga gct ttg gca atg aag ctg gat gat atg att 528
 Leu Leu Glu Thr Asn Arg Ala Leu Ala Met Lys Leu Asp Asp Met Ile
 165 170 175
 ggt gtg aga agt cat cat atg gga gga tgg gaa ggc ggt gaa cag aat 576
 Gly Val Arg Ser His His Met Gly Gly Trp Glu Gly Gly Glu Gln Asn
 180 185 190

gtt acc tac gcg cat cat caa gct cag tct cag gga cta tac cag cct 624
 Val Thr Tyr Ala His His Gln Ala Gln Ser Gln Gly Leu Tyr Gln Pro
 195 200 205
 ctt gaa tgc aat cca act ctg caa atg ggg tat gat aat cca gta tgc 672
 Leu Glu Cys Asn Pro Thr Leu Gln Met Gly Tyr Asp Asn Pro Val Cys
 210 215 220
 tct gag caa atc act gcg aca aca caa gct cag gcg cag ccg gga aac 720
 Ser Glu Gln Ile Thr Ala Thr Thr Gln Ala Gln Ala Gln Pro Gly Asn
 225 230 235 240
 ggt tac att cca gga tgg atg ctc tga 747
 Gly Tyr Ile Pro Gly Trp Met Leu
 245

<210> 28
 <211> 248
 <212> PRT
 <213> *Arabidopsis thaliana*

<220>
 <223> SEPALLATA1 (SEP1)

<400> 28
 Met Gly Arg Gly Arg Val Glu Leu Lys Arg Ile Glu Asn Lys Ile Asn
 1 5 10 15
 Arg Gln Val Thr Phe Ala Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Ile Phe
 35 40 45
 Ser Asn Arg Gly Lys Leu Tyr Glu Phe Cys Ser Ser Asn Met Leu
 50 55 60
 Lys Thr Leu Asp Arg Tyr Gln Lys Cys Ser Tyr Gly Ser Ile Glu Val
 65 70 75 80
 Asn Asn Lys Pro Ala Lys Glu Leu Glu Asn Ser Tyr Arg Glu Tyr Leu
 85 90 95
 Lys Leu Lys Gly Arg Tyr Glu Asn Leu Gln Arg Gln Gln Asn Leu
 100 105 110
 Leu Gly Glu Asp Leu Gly Pro Leu Asn Ser Lys Glu Leu Glu Gln Leu
 115 120 125
 Glu Arg Gln Leu Asp Gly Ser Leu Lys Gln Val Arg Ser Ile Lys Thr
 130 135 140
 Gln Tyr Met Leu Asp Gln Leu Ser Asp Leu Gln Asn Lys Glu Gln Met
 145 150 155 160
 Leu Leu Glu Thr Asn Arg Ala Leu Ala Met Lys Leu Asp Asp Met Ile
 165 170 175
 Gly Val Arg Ser His His Met Gly Gly Trp Glu Gly Gly Glu Gln Asn
 180 185 190
 Val Thr Tyr Ala His His Gln Ala Gln Ser Gln Gly Leu Tyr Gln Pro
 195 200 205
 Leu Glu Cys Asn Pro Thr Leu Gln Met Gly Tyr Asp Asn Pro Val Cys
 210 215 220
 Ser Glu Gln Ile Thr Ala Thr Thr Gln Ala Gln Ala Gln Pro Gly Asn
 225 230 235 240
 Gly Tyr Ile Pro Gly Trp Met Leu
 245

<210> 29
 <211> 753
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(753)
 <223> SEPALLATA2 (SEP2)

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<400> 29
atg gga aga gga aga gta gag ctc aag agg ata gag aac aaa atc aac 48
Met Gly Arg Gly Arg Val Glu Leu Lys Arg Ile Glu Asn Lys Ile Asn
  1             5             10             15

aga caa gtg acg ttt gct aaa cgt aga aat ggt ttg ctg aaa aaa gct 96
Arg Gln Val Thr Phe Ala Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
          20             25             30

tat gag ctt tct gtt ctc tgc gat gct gaa gtc tct ctc atc gtc ttc 144
Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ser Leu Ile Val Phe
          35             40             45

tcc aac cgt ggc aag ctc tac gag ttc tgc agc acc tcc aac atg ctc 192
Ser Asn Arg Gly Lys Leu Tyr Glu Phe Cys Ser Thr Ser Asn Met Leu
          50             55             60

aag aca ctg gaa agg tat cag aag tgt agc tat ggc tcc att gaa gtc 240
Lys Thr Leu Glu Arg Tyr Gln Lys Cys Ser Tyr Gly Ser Ile Glu Val
          65             70             75             80

aac aac aaa cct gct aaa gag ctt gag aac agc tac aga gag tac ttg 288
Asn Asn Lys Pro Ala Lys Glu Leu Glu Asn Ser Tyr Arg Glu Tyr Leu
          85             90             95

aag ctg aaa ggt aga tat gaa aat ctg caa cgt cag cag aga aat ctt 336
Lys Leu Lys Gly Arg Tyr Glu Asn Leu Gln Arg Gln Gln Arg Asn Leu
          100             105             110

ctt gga gag gat ctt gga cct ctg aat tca aag gag cta gag cag ctt 384
Leu Gly Glu Asp Leu Gly Pro Leu Asn Ser Lys Glu Leu Glu Gln Leu
          115             120             125

gag cgt caa cta gac ggc tct ctg aag caa gtt cgc tgc atc aag aca 432
Glu Arg Gln Leu Asp Gly Ser Leu Lys Gln Val Arg Cys Ile Lys Thr
          130             135             140

cag tat atg ctt gac cag ctc tct gat ctt caa ggt aag gag cat atc 480
Gln Tyr Met Leu Asp Gln Leu Ser Asp Leu Gln Gly Lys Glu His Ile
          145             150             155             160

ttg ctt gat gcc aac aga gct ttg tca atg aag ctg gaa gat atg atc 528
Leu Leu Asp Ala Asn Arg Ala Leu Ser Met Lys Leu Glu Asp Met Ile
          165             170             175

ggc gtg aga cat cac cat ata gga gga gga tgg gaa ggt ggt gat caa 576
Gly Val Arg His His His Ile Gly Gly Gly Trp Glu Gly Gly Asp Gln
          180             185             190

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cag aat att gcc tat gga cat cct cag gct cat tct cag gga cta tac 624
 Gln Asn Ile Ala Tyr Gly His Pro Gln Ala His Ser Gln Gly Leu Tyr
 195 200 205

 caa tct ctt gaa tgt gat ccc act ttg caa att gga tat agc cat cca 672
 Gln Ser Leu Glu Cys Asp Pro Thr Leu Gln Ile Gly Tyr Ser His Pro
 210 215 220

 gtg tgc tca gag caa atg gct gtg acg gtg caa ggt cag tcc caa caa 720
 Val Cys Ser Glu Gln Met Ala Val Thr Val Gln Gly Gln Ser Gln Gln
 225 230 235 240

 gga aac ggc tac atc cct ggc tgg atg ctg tga 753
 Gly Asn Gly Tyr Ile Pro Gly Trp Met Leu
 245 250

<210> 30
 <211> 250
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> SEPALLATA2 (SEP2)

<400> 30
 Met Gly Arg Gly Arg Val Glu Leu Lys Arg Ile Glu Asn Lys Ile Asn
 1 5 10 15
 Arg Gln Val Thr Phe Ala Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ser Leu Ile Val Phe
 35 40 45
 Ser Asn Arg Gly Lys Leu Tyr Glu Phe Cys Ser Thr Ser Asn Met Leu
 50 55 60
 Lys Thr Leu Glu Arg Tyr Gln Lys Cys Ser Tyr Gly Ser Ile Glu Val
 65 70 75 80
 Asn Asn Lys Pro Ala Lys Glu Leu Glu Asn Ser Tyr Arg Glu Tyr Leu
 85 90 95
 Lys Leu Lys Gly Arg Tyr Glu Asn Leu Gln Arg Gln Gln Arg Asn Leu
 100 105 110
 Leu Gly Glu Asp Leu Gly Pro Leu Asn Ser Lys Glu Leu Glu Gln Leu
 115 120 125
 Glu Arg Gln Leu Asp Gly Ser Leu Lys Gln Val Arg Cys Ile Lys Thr
 130 135 140
 Gln Tyr Met Leu Asp Gln Leu Ser Asp Leu Gln Gly Lys Glu His Ile
 145 150 155 160
 Leu Leu Asp Ala Asn Arg Ala Leu Ser Met Lys Leu Glu Asp Met Ile
 165 170 175
 Gly Val Arg His His His Ile Gly Gly Gly Trp Glu Gly Gly Asp Gln
 180 185 190
 Gln Asn Ile Ala Tyr Gly His Pro Gln Ala His Ser Gln Gly Leu Tyr
 195 200 205
 Gln Ser Leu Glu Cys Asp Pro Thr Leu Gln Ile Gly Tyr Ser His Pro
 210 215 220
 Val Cys Ser Glu Gln Met Ala Val Thr Val Gln Gly Gln Ser Gln Gln
 225 230 235 240
 Gly Asn Gly Tyr Ile Pro Gly Trp Met Leu
 245 250

<210> 31
 <211> 714
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(714)
 <223> SEPALLATA3 (SEP3)

<400> 31
 atg gga aga ggg aga gta gaa ttg aag agg ata gag aac aag atc aat 48
 Met Gly Arg Gly Arg Val Glu Leu Lys Arg Ile Glu Asn Lys Ile Asn
 1 5 10 15
 agg caa gtg acg ttt gca aag aga agg aat ggt ctt ttg aag aaa gca 96
 Arg Gln Val Thr Phe Ala Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
 20 25 30
 tac gag ctt tca gtt cta tgt gat gca gaa gtt gct ctc atc atc ttc 144
 Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Ile Phe
 35 40 45
 tca aat aga gga aag ctg tac gag ttt tgc agt agt tcg agc atg ctt 192
 Ser Asn Arg Gly Lys Leu Tyr Glu Phe Cys Ser Ser Ser Ser Met Leu
 50 55 60
 cgg aca ctg gag agg tac caa aag tgt aac tat gga gca cca gaa ccc 240
 Arg Thr Leu Glu Arg Tyr Glu Lys Cys Asn Tyr Gly Ala Pro Glu Pro
 65 70 75 80
 aat gtg cct tca aga gag gcc tta gca gtt gaa ctt agt agc cag cag 288
 Asn Val Pro Ser Arg Glu Ala Leu Ala Val Glu Leu Ser Ser Gln Gln
 85 90 95
 gag tat ctc aag ctt aag gag cgt tat gac gcc tta caa aga acc caa 336
 Glu Tyr Leu Lys Leu Lys Glu Arg Tyr Asp Ala Leu Gln Arg Thr Gln
 100 105 110
 agg aat ctg ttg gga gaa gat ctt gga cct cta agt aca aag gag ctt 384
 Arg Asn Leu Leu Gly Glu Asp Leu Gly Pro Leu Ser Thr Lys Glu Leu
 115 120 125
 gag tca ctt gag aga cag ctt gat tct tcc ttg aag cag atc aga gct 432
 Glu Ser Leu Glu Arg Gln Leu Asp Ser Ser Leu Lys Gln Ile Arg Ala
 130 135 140
 ctc agg aca cag ttt atg ctt gac cag ctc aac gat ctt cag agt aag 480
 Leu Arg Thr Gln Phe Met Leu Asp Gln Leu Asn Asp Leu Gln Ser Lys
 145 150 155 160
 tta gct gat ggg tat cag atg cca ctc cag ctg aac cct aac caa gaa 528
 Leu Ala Asp Gly Tyr Gln Met Pro Leu Gln Leu Asn Pro Asn Gln Glu
 165 170 175
 gag gtt gat cac tac ggt cgt cat cat cat caa caa caa caa cac tcc 576
 Glu Val Asp His Tyr Gly Arg His His His Gln Gln Gln Gln His Ser
 180 185 190

caa gct ttc ttc cag cct ttg gaa tgt gaa ccc att ctt cag atc ggg 624
 Gln Ala Phe Phe Gln Pro Leu Glu Cys Glu Pro Ile Leu Gln Ile Gly
 195 200 205

tat cag ggg cag caa gat gga atg gga gca gga cca agt gtg aat aat 672
 Tyr Gln Gly Gln Gln Asp Gly Met Gly Ala Gly Pro Ser Val Asn Asn
 210 215 220

tac atg ttg ggt tgg tta cct tat gac acc aac tct att tga 714
 Tyr Met Leu Gly Trp Leu Pro Tyr Asp Thr Asn Ser Ile
 225 230 235

<210> 32
 <211> 237
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> SEPALLATA3 (SEP3)

<400> 32
 Met Gly Arg Gly Arg Val Glu Leu Lys Arg Ile Glu Asn Lys Ile Asn
 1 5 10 15
 Arg Gln Val Thr Phe Ala Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Ile Phe
 35 40 45
 Ser Asn Arg Gly Lys Leu Tyr Glu Phe Cys Ser Ser Ser Ser Met Leu
 50 55 60
 Arg Thr Leu Glu Arg Tyr Gln Lys Cys Asn Tyr Gly Ala Pro Glu Pro
 65 70 75 80
 Asn Val Pro Ser Arg Glu Ala Leu Ala Val Glu Leu Ser Ser Gln Gln
 85 90 95
 Glu Tyr Leu Lys Leu Lys Glu Arg Tyr Asp Ala Leu Gln Arg Thr Gln
 100 105 110
 Arg Asn Leu Leu Gly Glu Asp Leu Gly Pro Leu Ser Thr Lys Glu Leu
 115 120 125
 Glu Ser Leu Glu Arg Gln Leu Asp Ser Ser Leu Lys Gln Ile Arg Ala
 130 135 140
 Leu Arg Thr Gln Phe Met Leu Asp Gln Leu Asn Asp Leu Gln Ser Lys
 145 150 155 160
 Leu Ala Asp Gly Tyr Gln Met Pro Leu Gln Leu Asn Pro Asn Gln Glu
 165 170 175
 Glu Val Asp His Tyr Gly Arg His His Gln Gln Gln Gln His Ser
 180 185 190
 Gln Ala Phe Phe Gln Pro Leu Glu Cys Glu Pro Ile Leu Gln Ile Gly
 195 200 205
 Tyr Gln Gly Gln Gln Asp Gly Met Gly Ala Gly Pro Ser Val Asn Asn
 210 215 220
 Tyr Met Leu Gly Trp Leu Pro Tyr Asp Thr Asn Ser Ile
 225 230 235

<210> 33
 <211> 645
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1) .. (645)
 <223> AGL20 (SUPPRESSOR OF CONSTANS (CO) OVEREXPRESSION
 1 (SOC1))

<400> 33

atg gtg agg ggc aaa act cag atg aag aga ata gag aat gca aca agc	48
Met Val Arg Gly Lys Thr Gln Met Lys Arg Ile Glu Asn Ala Thr Ser	
1 5 10 15	
aga caa gtg act ttc tcc aaa aga agg aat ggt ttg ttg aag aaa gcc	96
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala	
20 25 30	
ttt gag ctc tca gtg ctt tgt gat gct gaa gtt tct ctt atc atc ttc	144
Phe Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ser Leu Ile Ile Phe	
35 40 45	
tct cct aaa ggc aaa ctt tat gaa ttc gcc agc tcc aat atg caa gat	192
Ser Pro Lys Gly Lys Leu Tyr Glu Phe Ala Ser Ser Asn Met Gln Asp	
50 55 60	
acc ata gat cgt tat ctg agg cat act aag gat cga gtc agc acc aaa	240
Thr Ile Asp Arg Tyr Leu Arg His Thr Lys Asp Arg Val Ser Thr Lys	
65 70 75 80	
ccg gtt tct gaa gaa aat atg cag cat ttg aaa tat gaa gca gca aac	288
Pro Val Ser Glu Glu Asn Met Gln His Leu Lys Tyr Glu Ala Ala Asn	
85 90 95	
atg atg aag aaa att gaa caa ctc gaa gct tct aaa cgt aaa ctc ttg	336
Met Met Lys Lys Ile Glu Gln Leu Glu Ala Ser Lys Arg Lys Leu Leu	
100 105 110	
gga gaa ggc ata gga aca tgc tca atc gag gag ctg caa cag att gag	384
Gly Glu Gly Ile Gly Thr Cys Ser Ile Glu Glu Leu Gln Gln Ile Glu	
115 120 125	
caa cag ctt gag aaa agt gtc aaa tgt att cga gca aga aag act caa	432
Gln Gln Leu Glu Lys Ser Val Lys Cys Ile Arg Ala Arg Lys Thr Gln	
130 135 140	
gtg ttt aag gaa caa att gag cag ctc aag caa aag gag aaa gct cta	480
Val Phe Lys Glu Gln Ile Glu Gln Leu Lys Gln Lys Glu Lys Ala Leu	
145 150 155 160	
gct gca gaa aac gag aag ctc tct gaa aag tgg gga tct cat gaa agc	528
Ala Ala Glu Asn Glu Lys Leu Ser Glu Lys Trp Gly Ser His Glu Ser	
165 170 175	
gaa gtt tgg tca aat aag aat caa gaa agt act gga aga ggt gat gaa	576
Glu Val Trp Ser Asn Lys Asn Gln Glu Ser Thr Gly Arg Gly Asp Glu	
180 185 190	
gag agt agc cca agt tct gaa gta gag acg caa ttg ttc att ggg tta	624
Glu Ser Ser Pro Ser Ser Glu Val Glu Thr Gln Leu Phe Ile Gly Leu	
195 200 205	

cct tgt tct tca aga aag tga
 Pro Cys Ser Ser Arg Lys
 210 215

645

<210> 34
 <211> 214
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> AGL20 (SUPPRESSOR OF CONSTANS (CO) OVEREXPRESSION
 1 (SOC1))

<400> 34
 Met Val Arg Gly Lys Thr Gln Met Lys Arg Ile Glu Asn Ala Thr Ser
 1 5 10 15
 Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
 20 25 30
 Phe Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ser Leu Ile Ile Phe
 35 40 45
 Ser Pro Lys Gly Lys Leu Tyr Glu Phe Ala Ser Ser Asn Met Gln Asp
 50 55 60
 Thr Ile Asp Arg Tyr Leu Arg His Thr Lys Asp Arg Val Ser Thr Lys
 65 70 75 80
 Pro Val Ser Glu Glu Asn Met Gln His Leu Lys Tyr Glu Ala Ala Asn
 85 90 95
 Met Met Lys Lys Ile Glu Gln Leu Glu Ala Ser Lys Arg Lys Leu Leu
 100 105 110
 Gly Glu Gly Ile Gly Thr Cys Ser Ile Glu Glu Leu Gln Gln Ile Glu
 115 120 125
 Gln Gln Leu Glu Lys Ser Val Lys Cys Ile Arg Ala Arg Lys Thr Gln
 130 135 140
 Val Phe Lys Glu Gln Ile Glu Gln Leu Lys Gln Lys Glu Lys Ala Leu
 145 150 155 160
 Ala Ala Glu Asn Glu Lys Leu Ser Glu Lys Trp Gly Ser His Glu Ser
 165 170 175
 Glu Val Trp Ser Asn Lys Asn Gln Glu Ser Thr Gly Arg Gly Asp Glu
 180 185 190
 Glu Ser Ser Pro Ser Ser Glu Val Glu Thr Gln Leu Phe Ile Gly Leu
 195 200 205
 Pro Cys Ser Ser Arg Lys
 210

<210> 35
 <211> 633
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(633)
 <223> AGL22 (SHORT VEGETATIVE PHASE (SVP))

<220>
 <221> modified_base
 <222> (213)
 <223> n = g, a, c or t

<400> 35

atg gcg aga gaa aag att cag atc agg aag atc gac aac gca acg gcg	48
Met Ala Arg Glu Lys Ile Gln Ile Arg Lys Ile Asp Asn Ala Thr Ala	
1 5 10 15	
aga caa gtg acg ttt tcg aaa cga aga aga ggg ctt ttc aag aaa gct	96
Arg Gln Val Thr Phe Ser Lys Arg Arg Gly Leu Phe Lys Lys Ala	
20 25 30	
gaa gaa ctc tcc gtt ctc tgc gac gcc gat gtc gct ctc atc atc ttc	144
Glu Glu Leu Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Ile Phe	
35 40 45	
tct tcc acc gga aaa ctg ttc gag ttc tgt agc tcc agc atg aag gaa	192
Ser Ser Thr Gly Lys Leu Phe Glu Phe Cys Ser Ser Ser Met Lys Glu	
50 55 60	
gtc cta gag agg cat aac ttn cag tca aag aac ttg gag aag ctt cat	240
Val Leu Glu Arg His Asn Xaa Gln Ser Lys Asn Leu Glu Lys Leu His	
65 70 75 80	
cag cca tct ctt gag tta cag ctg gtt gag aac agt gat cac gcc cga	288
Gln Pro Ser Leu Glu Leu Gln Leu Val Glu Asn Ser Asp His Ala Arg	
85 90 95	
atg agt aaa gaa att gcg gac aag agc cac cga cta agg caa atg aga	336
Met Ser Lys Glu Ile Ala Asp Lys Ser His Arg Leu Arg Gln Met Arg	
100 105 110	
gga gag gaa ctt caa gga ctt gac att gaa gag ctt cag cag cta gag	384
Gly Glu Glu Leu Gln Gly Leu Asp Ile Glu Glu Leu Gln Gln Leu Glu	
115 120 125	
aag gcc ctt gaa act ggt ttg acg cgt gtg att gaa aca aag agt gac	432
Lys Ala Leu Glu Thr Gly Leu Thr Arg Val Ile Glu Thr Lys Ser Asp	
130 135 140	
aag att atg agt gag atc agc gaa ctt cag aaa aag gga atg caa ttg	480
Lys Ile Met Ser Glu Ile Ser Glu Leu Gln Lys Lys Gly Met Gln Leu	
145 150 155 160	
atg gat gag aac aag cgg ttg agg cag caa gta tgt gtc tta ccc tct	528
Met Asp Glu Asn Lys Arg Leu Arg Gln Gln Val Cys Val Leu Pro Ser	
165 170 175	
ctg ttg ata aca aat ccc ttt ctt ttg tct acc att aac gta cac act	576
Leu Leu Ile Thr Asn Pro Phe Leu Leu Ser Thr Ile Asn Val His Thr	
180 185 190	
cct aaa ttt aat ccc cag ttg tct aca aca cat atg ttt gat cat act	624
Pro Lys Phe Asn Pro Gln Leu Ser Thr Thr His Met Phe Asp His Thr	
195 200 205	
gtg aga taa	633
Val Arg	
210	

<210> 36
 <211> 210
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> AGL22 (SHORT VEGETATIVE PHASE (SVP))

<220>
 <221> MOD_RES
 <222> (71)
 <223> Xaa = Phe or Leu

<400> 36
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 1 5 10 15
 Arg Gln Val Thr Phe Ser Lys Arg Arg Gly Leu Phe Lys Lys Ala
 20 25 30
 Glu Glu Leu Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Ile Phe
 35 40 45
 Ser Ser Thr Gly Lys Leu Phe Glu Phe Cys Ser Ser Ser Met Lys Glu
 50 55 60
 Val Leu Glu Arg His Asn Xaa Gln Ser Lys Asn Leu Glu Lys Leu His
 65 70 75 80
 Gln Pro Ser Leu Glu Leu Gln Leu Val Glu Asn Ser Asp His Ala Arg
 85 90 95
 Met Ser Lys Glu Ile Ala Asp Lys Ser His Arg Leu Arg Gln Met Arg
 100 105 110
 Gly Glu Glu Leu Gln Gly Leu Asp Ile Glu Glu Leu Gln Gln Leu Glu
 115 120 125
 Lys Ala Leu Glu Thr Gly Leu Thr Arg Val Ile Glu Thr Lys Ser Asp
 130 135 140
 Lys Ile Met Ser Glu Ile Ser Glu Leu Gln Lys Lys Gly Met Gln Leu
 145 150 155 160
 Met Asp Glu Asn Lys Arg Leu Arg Gln Gln Val Cys Val Leu Pro Ser
 165 170 175
 Leu Leu Ile Thr Asn Pro Phe Leu Leu Ser Thr Ile Asn Val His Thr
 180 185 190
 Pro Lys Phe Asn Pro Gln Leu Ser Thr Thr His Met Phe Asp His Thr
 195 200 205
 Val Arg
 210

<210> 37
 <211> 663
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(663)
 <223> AGL24

<400> 37
 atg gcg aga gag aag ata agg ata aag aag att gat aac ata aca gcg 48
 Met Ala Arg Glu Lys Ile Arg Ile Lys Lys Ile Asp Asn Ile Thr Ala
 1 5 10 15

aga caa gtt act ttc tca aag aga aga aga gga atc ttc aag aaa gcc	96
Arg Gln Val Thr Phe Ser Lys Arg Arg Arg Gly Ile Phe Lys Lys Ala	
20 25 30	
gat gaa ctt tca gtt ctt tgc gat gct gat gtt gct ctc atc atc ttc	144
Asp Glu Leu Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Ile Phe	
35 40 45	
tct gcc acc gga aag ctc ttc gag ttc tcc agc tca aga atg aga gac	192
Ser Ala Thr Gly Lys Leu Phe Glu Phe Ser Ser Ser Arg Met Arg Asp	
50 55 60	
ata ttg gga agg tat agt ctt cat gca agt aac atc aac aaa ttg atg	240
Ile Leu Gly Arg Tyr Ser Leu His Ala Ser Asn Ile Asn Lys Leu Met	
65 70 75 80	
gat cca cct tct act cat ctc cgg ctt gag aat tgt aac ctc tcc aga	288
Asp Pro Pro Ser Thr His Leu Arg Leu Glu Asn Cys Asn Leu Ser Arg	
85 90 95	
cta agt aag gaa gtc gaa gac aaa acc aag cag cta cgg aaa ctg aga	336
Leu Ser Lys Glu Val Glu Asp Lys Thr Lys Gln Leu Arg Lys Leu Arg	
100 105 110	
gga gag gat ctt gat gga ttg aac tta gaa gag ttg cag cgg ctg gag	384
Gly Glu Asp Leu Asp Gly Leu Asn Leu Glu Glu Leu Gln Arg Leu Glu	
115 120 125	
aaa cta ctt gaa tcc gga ctt agc cgt gtg tct gaa aag aag ggc gag	432
Lys Leu Leu Glu Ser Gly Leu Ser Arg Val Ser Glu Lys Lys Gly Glu	
130 135 140	
tgt gtg atg agc caa att ttc tca ctt gag aaa cgg gga tcg gaa ttg	480
Cys Val Met Ser Gln Ile Phe Ser Leu Glu Lys Arg Gly Ser Glu Leu	
145 150 155 160	
gtg gat gag aat aag aga ctg agg gat aaa cta gag acg ttg gaa agg	528
Val Asp Glu Asn Lys Arg Leu Arg Asp Lys Leu Glu Thr Leu Glu Arg	
165 170 175	
gca aaa ctg acg acg ctt aaa gag gct ttg gag aca gag tcg gtg acc	576
Ala Lys Leu Thr Thr Leu Lys Glu Ala Leu Glu Thr Glu Ser Val Thr	
180 185 190	
aca aat gtg tca agc tac gac agt gga act ccc ctt gag gat gac tcc	624
Thr Asn Val Ser Ser Tyr Asp Ser Gly Thr Pro Leu Glu Asp Asp Ser	
195 200 205	
gac act tcc ctg aag ctt ggg ctt cca tct tgg gaa tga	663
Asp Thr Ser Leu Lys Leu Gly Leu Pro Ser Trp Glu	
210 215 220	

<210> 38

<211> 220

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> AGL24

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<400> 38
Met Ala Arg Glu Lys Ile Arg Ile Lys Lys Ile Asp Asn Ile Thr Ala
 1          5          10          15
Arg Gln Val Thr Phe Ser Lys Arg Arg Gly Ile Phe Lys Lys Ala
 20          25          30
Asp Glu Leu Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Ile Phe
 35          40          45
Ser Ala Thr Gly Lys Leu Phe Glu Phe Ser Ser Ser Arg Met Arg Asp
 50          55          60
Ile Leu Gly Arg Tyr Ser Leu His Ala Ser Asn Ile Asn Lys Leu Met
 65          70          75          80
Asp Pro Pro Ser Thr His Leu Arg Leu Glu Asn Cys Asn Leu Ser Arg
 85          90          95
Leu Ser Lys Glu Val Glu Asp Lys Thr Lys Gln Leu Arg Lys Leu Arg
 100         105         110
Gly Glu Asp Leu Asp Gly Leu Asn Leu Glu Glu Leu Gln Arg Leu Glu
 115         120         125
Lys Leu Leu Glu Ser Gly Leu Ser Arg Val Ser Glu Lys Lys Gly Glu
 130         135         140
Cys Val Met Ser Gln Ile Phe Ser Leu Glu Lys Arg Gly Ser Glu Leu
 145         150         155         160
Val Asp Glu Asn Lys Arg Leu Arg Asp Lys Leu Glu Thr Leu Glu Arg
 165         170         175
Ala Lys Leu Thr Thr Leu Lys Glu Ala Leu Glu Thr Glu Ser Val Thr
 180         185         190
Thr Asn Val Ser Ser Tyr Asp Ser Gly Thr Pro Leu Glu Asp Asp Ser
 195         200         205
Asp Thr Ser Leu Lys Leu Gly Leu Pro Ser Trp Glu
 210         215         220

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<210> 39
<211> 687
<212> DNA
<213> Arabidopsis thaliana

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<220>
<221> CDS
<222> (1)..(687)
<223> AGL27

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<400> 39
atg gga aga aga aaa atc gag atc aag cga atc gag aac aaa agc agt      48
Met Gly Arg Arg Lys Ile Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
 1          5          10          15

cga caa gtc act ttc tcc aaa cga cgc aat ggt ctc atc gac aaa gct      96
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Asp Lys Ala
 20          25          30

cga caa ctt tcg att ctc tgt gaa tcc tcc gtc gct gtt gtc gtc gta     144
Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Val Ala Val Val Val Val
 35          40          45

tct gcc tcc gga aaa ctc tat gac tct tcc tcc ggt gac gac att tcc     192
Ser Ala Ser Gly Lys Leu Tyr Asp Ser Ser Ser Gly Asp Asp Ile Ser
 50          55          60

aag atc att gat cgt tat gaa ata caa cat gct gat gaa ctt aga gcc     240
Lys Ile Ile Asp Arg Tyr Glu Ile Gln His Ala Asp Glu Leu Arg Ala
 65          70          75          80

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tta gat ctt gaa gaa aaa att cag aat tat ctt cca cac aag gag tta	288
Leu Asp Leu Glu Glu Lys Ile Gln Asn Tyr Leu Pro His Lys Glu Leu	
85 90 95	
cta gaa aca gtc caa agc aag ctt gaa gaa cca aat gtc gat aat gta	336
Leu Glu Thr Val Gln Ser Lys Leu Glu Glu Pro Asn Val Asp Asn Val	
100 105 110	
agt gta gat tct cta att tct ctg gag gaa caa ctt gag act gct ctg	384
Ser Val Asp Ser Leu Ile Ser Leu Glu Glu Gln Leu Glu Thr Ala Leu	
115 120 125	
tcc gta agt aga gct agg aag gca gaa ctg atg atg gag tat atc gag	432
Ser Val Ser Arg Ala Arg Lys Ala Glu Leu Met Met Glu Tyr Ile Glu	
130 135 140	
tcc ctt aaa gaa aag gag aaa ttg ctg aga gaa gag aac cag gtt ctg	480
Ser Leu Lys Glu Lys Glu Lys Leu Leu Arg Glu Glu Asn Gln Val Leu	
145 150 155 160	
gct agc cag ctg tca gag aag aaa ggt atg tct cac cga tga aag ata	528
Ala Ser Gln Leu Ser Glu Lys Lys Gly Met Ser His Arg Lys Ile	
165 170 175	
ctc aaa acc cga tgg gaa aga ata cgt tgc tgg caa cag atg atg aga	576
Leu Lys Thr Arg Trp Glu Arg Ile Arg Cys Trp Gln Gln Met Met Arg	
180 185 190	
gag gaa tgt ttc cgg gaa gta gct ccg gca aca aaa tac cgg aga ctc	624
Glu Glu Cys Phe Arg Glu Val Ala Pro Ala Thr Lys Tyr Arg Arg Leu	
195 200 205	
tcc cgc tgc tca att agc cac cat cat caa cgg ctg agt ttt cac ctt	672
Ser Arg Cys Ser Ile Ser His His His Gln Arg Leu Ser Phe His Leu	
210 215 220	
aaa ctc aaa gcc tga	687
Lys Leu Lys Ala	
225	

<210> 40

<211> 173

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> AGL27

<400> 40

Met Gly Arg Arg Lys Ile Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser	
1 5 10 15	
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Asp Lys Ala	
20 25 30	
Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Val Ala Val Val Val	
35 40 45	
Ser Ala Ser Gly Lys Leu Tyr Asp Ser Ser Ser Gly Asp Asp Ile Ser	
50 55 60	
Lys Ile Ile Asp Arg Tyr Glu Ile Gln His Ala Asp Glu Leu Arg Ala	
65 70 75 80	

caatccaaaa	ataaatatgt	tccactcttt	tggttagcgt	ttaactaaag	atgcgtttta	1200
ctttatgtaa	gtgggtgatc	ttttggcaat	gggggacaat	gactatacaa	tctaagagat	1260
catttttaacg	aatatcattc	atatttcatc	ctcttcttca	aatttcagtt	tactaatta	1320
accacgtttc	aattgtagtg	tatcgcgagc	tgtaaatatt	atctaattta	tgttacataa	1380
tcataactgt	aatctttatt	agacaaaaac	atatatacct	cactgcaaac	accttcaaac	1440
atggataaact	tgattttaggc	atacaaatat	tatttctcat	ttatttgata	tgacctatat	1500
tatgtggcta	ttttatcagt	tttagtggtt	tttatgataa	ttgaaccact	taaaatgttt	1560
tctcattttt	caattttatt	taaactgaat	taaaaagtaa	gaaagtatga	tccaataagg	1620
catcgacaca	tggaaaccca	ttttaaggta	gaagatgctt	ttctgagggt	tctgaaaaaca	1680
actagaaaaa	gatatgatac	gttgctttca	tttattgtaa	gtattattta	gttttaattc	1740
acgcgcttca	tatccagctg	caagactact	acaacttgca	attatgagac	tctcgttaga	1800
aaattaccag	gtataattta	aaaacaaaaa	gaactagaat	atattggcaa	ttatttgaag	1860
taagaaaaata	tgagattctt	gaccgagttg	ttaaactatc	aaacccaaaa	gttttggtta	1920
aaaaataagc	tagtactatg	tacatatgtt	ttatgttgaa	aatatattaa	actgtatgta	1980
agagggagtg	tactttcatt	ttagatatac	atttccagct	agtagcaggt	ctctatatat	2040
aaactttctt	aatatcgcta	aacaaatttt	actttcaagt	ttgtaatgtg	ataagtgaag	2100
gaccgtatat	acatacacat	gttaactcaac	tgataacctt	gtgcctcgt	gtgtcagtt	2160
actagccaac	catcaaacgt	gcatgatgct	gtttttctta	gagtactatt	gttgtgttat	2220
atataactaa	acataaacia	tttgctatta	tgatataaac	atagaatttt	caagcaatga	2280
tatgtttaga	tgttttgtat	aaatattcca	taaatagtag	acacccatat	atacacaac	2340
atgaattcta	cctgaggaga	aacacataga	tgttcaaat	aaataataac	cctataatga	2400
aaactctaaa	gtaagtaata	cgaataaaaa	atttatcctt	taaaatacat	ataaacatat	2460
atatacaagt	ttatattgta	attgtatcac	aagagccaat	tatttgggta	ctgtatcaca	2520
cgtgcttaaa	ggagcgtgg	gaatgaaagt	aaagaagaat	aaagaagcag	agagatgggc	2580
tagaaatgag	aaaacacacc	aaaccctaac	ctcacctca	cacatttctt	atcttttgct	2640
ctcaatagat	tccattgatt	caaaacaaaa	ttttcattaa	gatttcacaa	cctccacaca	2700
cttccaaaca	caattaaaga	gaggaaaaag	aatcaataac	cctataaata	aaaaatcaga	2760
caaacagaag	tttctctctt	ttcttcttta	agctagtacc	ttttgttctt	gaaattaggg	2820
ttatatttctt	ttttccaaat	accatcaatt	ctccagacca	taaaaactca	aaaagatcag	2880
atctttctct	tgaaaaagag	atacccaact	tatgtttttg	tgtgtctgta	tatagataaa	2940
cattacatac	ccatatttgt	gtatagacat	aaaaagtgga	aattaaggta	acaaaaagaa	3000
atgggaagag	gaagagtga	gctgaagagg	atagagaaca	aatcaacag	acaagttaacg	3060
tttgcaaagc	gtaggaacgg	tttgttgaag	aaagcttatg	aattgtctgt	tctctgtgat	3120
gctgaagttg	ctctcatcat	cttctccaac	cgtggaaagc	tctatgagtt	ttgcagctcc	3180
tcaaagtaaa	caactctctc	actctttatc	gttttcttga	ttgagttttt	gctagatctg	3240
agcttagatc	tttgtctcaa	ggacttggtta	tatatagatc	acacgatctt	gatttctacg	3300
aagttgagtt	aattagattt	cttgatttca	ttttctaggg	tttttttcca	attcttgaaa	3360
tttaagatct	ggtttttttg	ttgtcaatga	tttagaactg	tgaattttgt	aatcgaaatg	3420
attccaaatc	ctgatatgca	atctgaaaag	ttttatataa	ttaatatatg	tctgtgtgat	3480
tggaacttta	aaagttgttc	acagatttct	atgaaaatta	caagtatcca	acgtagaatg	3540
ataatatatg	gttacatgca	ttaaccattt	gttagttcat	catactttat	gggtggttaa	3600
acttcaaagc	cgtgtatatc	tgtgaaggct	ttgattgttt	gttttttctt	aaaaacaatg	3660
tttaatagat	ttttaattat	atgtttaaata	agttttgctt	acatgcattc	aagaaaatat	3720
agcgattaat	tccttttttc	aatcacaat	ttgtgaatca	aacgaaaacg	taagatatgt	3780
cttgcaaagc	ataggattga	actattgata	tttgtaaata	taaatacgaa	actttacgtt	3840
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Lys Glu Lys Leu Leu Arg Glu Glu Asn Gln Val Leu Ala Ser Gln Met	
145 150 155 160	
Gly Lys Asn Thr Leu Leu Ala Thr Asp Asp Glu Arg Gly Met Phe Pro	
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Gly Ser Ser Ser Gly Asn Lys Ile Pro Glu Thr Leu Pro Leu Leu Asn	
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